

Errors Corrected by the STIC Systems Branch

Serial Number: 09/285,531A

CRF Processing Date: 10/17/2000
 Edited by: AKH
 Verified by: AKH (STIC staff)

ENTERED

OCT 25 2000

TECH CENTER 1600 2000

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☒ Other: Seqs 1-2 - moved C2207 response to C2237

***Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.**

3/1/95

Page 1 of 7
RECEIVED

OCT 25 2000

TECH CENTER 1800/2900

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/285,531A
DATE: 10/24/2000
TIME: 19:58:39

Input Set : A:\Pto.amc
Output Set: N:\CRF3\10242000\I285531A.raw

1 <110> APPLICANT: Chernajovsky, Yuti
2 Neve, Richard
3 Feldmann, Marc
5 <120> TITLE OF INVENTION: Small Molecular Weight TNF Receptor Multimeric Molecule
7 <130> FILE REFERENCE: KIR95-01A
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/285,531A
C--> 9 <141> CURRENT FILING DATE: 1999-04-02
9 <150> PRIOR APPLICATION NUMBER: 08/437,533
10 <151> PRIOR FILING DATE: 1995-05-09
12 <160> NUMBER OF SEQ ID NOS: 4
14 <170> SOFTWARE: FastSEQ for Windows Version 3.0
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 1506
18 <212> TYPE: DNA
19 <213> ORGANISM: Artificial Sequence
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (1)...(1506)
24 <223> OTHER INFORMATION: Open Reading Frame of Human P75 TNF-R ECD
26 <400> SEQUENCE: 1
27 atg gcg ccc gtc gcc gtc tgg gcc gcg ctg gcc gtc gga ctg gag ctc 48
28 Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu
29 1 5 10 15
31 tgg gct gcg gcg cac gcc ttg ccc gcc cag gtg gca ttt aca ccc tac 96
32 Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
33 20 25 30
35 gcc ccg gag ccc ggg agc aca tgc cgg ctc aga gaa tac tat gac cag 144
36 Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
37 35 40 45
39 aca gct cag atg tgc tgc agc aaa tgc tcg ccg ggc caa cat gca aaa 192
40 Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
41 50 55 60
43 gtc ttc tgt acc aag acc tcg gac acc gtg tgt gac tcc tgt gag gac 240
44 Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
45 65 70 75 80
47 agc aca tac acc cag ctc tgg aac tgg gtt ccc gag tgc ttg agc tgt 288
48 Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
49 85 90 95
52 ggc tcc cgc tgt agc tct gac cag gtg gaa act caa gcc tgc act cgg 336
53 Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
54 100 105 110
58 gaa cag aac cgc atc tgc acc tgc agg ccc ggc tgg tac tgc gcg ctg 384
59 Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
60 115 120 125
62 agc aag cag gag ggg tgc cgg ctg tgc gcg ccg ctg cgc aag tgc cgc 432
63 Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
64 130 135 140

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66	ccg ggc ttc ggc gtg gcc aga cca gga act gaa aca tca gac gtg gtg	480
67	Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val	
68	145 150 155 160	
70	tgc aag ccc tgt gcc ccg ggg acg ttc tcc aac acg act tca tcc acg	528
71	Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr	
72	165 170 175	
74	gat att tgc agg ccc cac cag atc tgt aac gtg gtg gcc atc cct ggg	576
75	Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly	
76	180 185 190	
78	aat gca agc atg gat gca gtc tgc acg tcc acg tcc ccc acc cgg agt	624
79	Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser	
80	195 200 205	
82	atg gcc cca ggg gca gta cac tta ccc cag cca gtg tcc aca cga tcc	672
83	Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser	
84	210 215 220	
86	caa cac acg cag cca act cca gaa ccc agc act gct cca agc acc tcc	720
87	Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser	
88	225 230 235 240	
90	ttc ctg ctc cca atg ggc ccc agc ccc cca gct aga ggt ggg ggc ggt	768
91	Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Arg Gly Gly Gly Gly	
92	245 250 255	
94	tcg ggt ggc ggc ggc tcg ggc ggg ggt ggc tcg gat ccc gcc cag gtg	816
95	Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Pro Ala Gln Val	
96	260 265 270	
98	gca ttt aca ccc tac gcc ccg gag ccc ggg agc aca tgc cgg ctc aga	864
99	Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg	
100	275 280 285	
102	gaa tac tat gac cag aca gct cag atg tgc tgc agc aaa tgc tcg ccg	912
103	Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro	
104	290 295 300	
106	ggc caa cat gca aaa gtc ttc tgt acc aag acc tcg gac acc gtg tgt	960
107	Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys	
108	305 310 315 320	
110	gac tcc tgt gag gac agc aca tac acc cag ctc tgg aac tgg gtt ccc	1008
111	Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro	
112	325 330 335	
114	gag tgc ttg agc tgt ggc tcc cgc tgt agc tct gac cag gtg gaa act	1056
115	Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr	
116	340 345 350	
118	caa gcc tgc act cgg gaa cag aac cgc atc tgc acc tgc agg ccc ggc	1104
119	Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly	
120	355 360 365	
122	tgg tac tgc gcg ctg agc aag cag gag ggg tgc cgg ctg tgc gcg ccg	1152
123	Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro	
124	370 375 380	
126	ctg cgc aag tgc cgc ccg ggc ttc ggc gtg gcc aga cca gga act gaa	1200
127	Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu	
128	385 390 395 400	
130	aca tca gac gtg gtg tgc aag ccc tgt gcc ccg ggg acg ttc tcc aac	1248

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131 Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn
132                               405                               410                               415
134 acg act tca tcc acg gat att tgc agg ccc cac cag atc tgt aac gtg      1296
135 Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val
136                               420                               425                               430
138 gtg gcc atc cct ggg aat gca agc atg gat gca gtc tgc acg tcc acg      1344
139 Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr
140                               435                               440                               445
142 tcc ccc acc cgg agt atg gcc cca ggg gca gta cac tta ccc cag cca      1392
143 Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val His Leu Pro Gln Pro
144                               450                               455                               460
146 gtg tcc aca cga tcc caa cac acg cag cca act cca gaa ccc agc act      1440
147 Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr
148 465                               470                               475                               480
150 gct cca agc acc tcc ttc ctg ctc cca atg ggc ccc agc ccc cca gct      1488
151 Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala
152                               485                               490                               495
154 gaa ggg agc act ggc tag      1506
155 Glu Gly Ser Thr Gly *
156                               500
159 <210> SEQ ID NO: 2
160 <211> LENGTH: 501
161 <212> TYPE: PRT
162 <213> ORGANISM: Artificial Sequence
164 <220> FEATURE:
165 <223> OTHER INFORMATION: Open Reading Frame of Human P75 TNF-R ECD
167 <400> SEQUENCE: 2
168 Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu
169 1 5 10 15
170 Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
171 20 25 30
172 Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
173 35 40 45
174 Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
175 50 55 60
177 Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
178 65 70 75 80
180 Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
181 85 90 95
182 Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
183 100 105 110
184 Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
185 115 120 125
186 Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
187 130 135 140
188 Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
189 145 150 155 160
190 Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
191 165 170 175

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192 Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
193      180      185      190
194 Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
195      195      200      205
196 Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
197      210      215      220
198 Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
199      225      230      235      240
200 Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Arg Gly Gly Gly Gly
201      245      250      255
202 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Pro Ala Gln Val
203      260      265      270
204 Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg
205      275      280      285
206 Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro
207      290      295      300
208 Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys
209      305      310      315      320
210 Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro
211      325      330      335
212 Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr
213      340      345      350
216 Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly
217      355      360      365
218 Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro
219      370      375      380
220 Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu
221      385      390      395      400
222 Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn
223      405      410      415
224 Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val
225      420      425      430
226 Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr
227      435      440      445
228 Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val His Leu Pro Gln Pro
229      450      455      460
230 Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr
231      465      470      475      480
232 Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala
233      485      490      495
234 Glu Gly Ser Thr Gly
235      500
237 <210> SEQ ID NO: 3
238 <211> LENGTH: 30
239 <212> TYPE: DNA
240 <213> ORGANISM: Artificial Sequence
242 <220> FEATURE:
243 <223> OTHER INFORMATION: deoxyoligonucleotide primer
245 <400> SEQUENCE: 3

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246  tcggatcccg cccaggtggc atttacaccc           30
248  <210> SEQ ID NO: 4
249  <211> LENGTH: 20
250  <212> TYPE: DNA
251  <213> ORGANISM: Artificial Sequence
253  <220> FEATURE:
254  <223> OTHER INFORMATION: deoxyoligonucleotide primer
256  <400> SEQUENCE: 4
257  cggaattcta gaaggtaccc           20
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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/285,531A

DATE: 10/24/2000

TIME: 19:58:40

Input Set : A:\Pto.amc

Output Set: N:\CRF3\10242000\I285531A.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date